

Vonda

RAW SEQUENCE LISTING

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Application Serial Number: 10/517,310
Source: PCT
Date Processed by STIC: 10/25/2005

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PCT

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DATE: 10/25/2005

PATENT APPLICATION: US/10/517,310

TIME: 12:04:15

Input Set : A:\262507US0PCT.txt

Output Set: N:\CRF4\10252005\J517310.raw

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3 <110> APPLICANT: KOTANI, HIDEHITO
4   MIZUARAI, SHINJI
6 <120> TITLE OF INVENTION: METHOD FOR PREDICTING A DRUG TRANSPORT CAPABILITY BY ABCG2
7   POLYMORPHISMS
9 <130> FILE REFERENCE: 262507US0PCT
11 <140> CURRENT APPLICATION NUMBER: 10/517,310
12 <141> CURRENT FILING DATE: 2004-12-17
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07534
15 <151> PRIOR FILING DATE: 2003-06-13
17 <150> PRIOR APPLICATION NUMBER: JP 2002-175806
18 <151> PRIOR FILING DATE: 2002-06-17
20 <160> NUMBER OF SEQ ID NOS: 68
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1968
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1965)
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37 1          5          10          15
39 acc aat ggc ttc ccc gcg aca gct tcc aat gac ctg aag gca ttt act      96
40 Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
41          20          25          30
43 gaa gga gct gtg tta agt ttt cat aac atc tgc tat cga gta aaa ctg      144
44 Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
45          35          40          45
47 aag agt ggc ttt cta cct tgt cga aaa cca gtt gag aaa gaa ata tta      192
48 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
49          50          55          60
51 tcg aat atc aat ggg atc atg aaa cct ggt ctc aac gcc atc ctg gga      240
52 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
53 65          70          75          80
55 ccc aca ggt gga ggc aaa tct tcg tta tta gat gtc tta gct gca agg      288
56 Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
57          85          90          95
59 aaa gat cca agt gga tta tct gga gat gtt ctg ata aat gga gca ccg      336
60 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
61          100          105          110
63 cga cct gcc aat ttc aaa tgt aat tca ggt tac gtg gta caa gat gat      384

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67	gtt	gtg	atg	ggc	act	ctg	acg	gtg	aga	gaa	aac	tta	cag	ttc	tca	gca	432
68	Val	Val	Met	Gly	Thr	Leu	Thr	Val	Arg	Glu	Asn	Leu	Gln	Phe	Ser	Ala	
69		130					135					140					
71	gct	ctt	cgg	ctt	gca	aca	act	atg	acg	aat	cat	gaa	aaa	aac	gaa	cgg	480
72	Ala	Leu	Arg	Leu	Ala	Thr	Thr	Met	Thr	Asn	His	Glu	Lys	Asn	Glu	Arg	
73	145					150					155				160		
75	att	aac	agg	gtc	att	caa	gag	tta	ggg	ctg	gat	aaa	gtg	gca	gac	tcc	528
76	Ile	Asn	Arg	Val	Ile	Gln	Glu	Leu	Gly	Leu	Asp	Lys	Val	Ala	Asp	Ser	
77			165							170				175			
79	aag	gtt	gga	act	cag	ttt	atc	cgt	ggg	gtg	tct	gga	gga	gaa	aga	aaa	576
80	Lys	Val	Gly	Thr	Gln	Phe	Ile	Arg	Gly	Val	Ser	Gly	Gly	Glu	Arg	Lys	
81			180					185					190				
83	agg	act	agt	ata	gga	atg	gag	ctt	atc	act	gat	cct	tcc	atc	ttg	ttc	624
84	Arg	Thr	Ser	Ile	Gly	Met	Glu	Leu	Ile	Thr	Asp	Pro	Ser	Ile	Leu	Phe	
85		195					200					205					
87	ttg	gat	gag	cct	aca	act	ggc	tta	gac	tca	agc	aca	gca	aat	gct	gtc	672
88	Leu	Asp	Glu	Pro	Thr	Thr	Gly	Leu	Asp	Ser	Ser	Thr	Ala	Asn	Ala	Val	
89		210					215					220					
91	ctt	ttg	ctc	ctg	aaa	agg	atg	tct	aag	cag	gga	cga	aca	atc	atc	ttc	720
92	Leu	Leu	Leu	Leu	Lys	Arg	Met	Ser	Lys	Gln	Gly	Arg	Thr	Ile	Ile	Phe	
93	225				230					235				240			
95	tcc	att	cat	cag	cct	cga	tat	tcc	atc	ttc	aag	ttg	ttt	gat	agc	ctc	768
96	Ser	Ile	His	Gln	Pro	Arg	Tyr	Ser	Ile	Phe	Lys	Leu	Phe	Asp	Ser	Leu	
97			245					250				255					
99	acc	tta	ttg	gcc	tca	gga	aga	ctt	atg	ttc	cac	ggg	cct	gct	cag	gag	816
100	Thr	Leu	Leu	Ala	Ser	Gly	Arg	Leu	Met	Phe	His	Gly	Pro	Ala	Gln	Glu	
101			260					265				270					
103	gcc	ttg	gga	tac	ttt	gaa	tca	gct	ggg	tat	cac	tgt	gag	gcc	tat	aat	864
104	Ala	Leu	Gly	Tyr	Phe	Glu	Ser	Ala	Gly	Tyr	His	Cys	Glu	Ala	Tyr	Asn	
105		275					280					285					
107	aac	cct	gca	gac	ttc	ttc	ttg	gac	atc	att	aat	gga	gat	tcc	act	gct	912
108	Asn	Pro	Ala	Asp	Phe	Phe	Leu	Asp	Ile	Ile	Asn	Gly	Asp	Ser	Thr	Ala	
109		290					295					300					
111	gtg	gca	tta	aac	aga	gaa	gaa	gac	ttt	aaa	gcc	aca	gag	atc	ata	gag	960
112	Val	Ala	Leu	Asn	Arg	Glu	Glu	Asp	Phe	Lys	Ala	Thr	Glu	Ile	Ile	Glu	
113	305				310					315			320				
115	cct	tcc	aag	cag	gat	aag	cca	ctc	ata	gaa	aaa	tta	gag	gag	att	tat	1008
116	Pro	Ser	Lys	Gln	Asp	Lys	Pro	Leu	Ile	Glu	Lys	Leu	Ala	Glu	Ile	Tyr	
117			325					330				335					
119	gtc	aac	tcc	tcc	ttc	tac	aaa	gag	aca	aaa	gct	gaa	tta	cat	caa	ctt	1056
120	Val	Asn	Ser	Ser	Phe	Tyr	Lys	Glu	Thr	Lys	Ala	Glu	Leu	His	Gln	Leu	
121			340					345				350					
123	tcc	ggg	ggg	gag	aag	aag	aag	aag	atc	aca	gtc	ttc	aag	gag	atc	agc	1104
124	Ser	Gly	Gly	Glu	Lys	Lys	Lys	Lys	Ile	Thr	Val	Phe	Lys	Glu	Ile	Ser	
125		355					360					365					
127	tac	acc	acc	tcc	ttc	tgt	cat	caa	ctc	aga	tgg	gtt	tcc	aag	cgt	tca	1152
128	Tyr	Thr	Thr	Ser	Phe	Cys	His	Gln	Leu	Arg	Trp	Val	Ser	Lys	Arg	Ser	

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132	Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile			
133	385 390 395 400			
135	gtc aca gtc gta ctg gga ctg gtt ata ggt gcc att tac ttt ggg cta	1248		
136	Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu			
137	405 410 415			
139	aaa aat gat tct act gga atc cag aac aga gct ggg gtt ctc ttc ttc	1296		
140	Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe			
141	420 425 430			
143	ctg acg acc aac cag tgt ttc agc agt gtt tca gcc gtg gaa ctc ttt	1344		
144	Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe			
145	435 440 445			
147	gtg gta gag aag aag ctc ttc ata cat gaa tac atc agc gga tac tac	1392		
148	Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr			
149	450 455 460			
151	aga gtg tca tct tat ttc ctt gga aaa ctg tta tct gat tta tta ccc	1440		
152	Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro			
153	465 470 475 480			
155	atg agg atg tta cca agt att ata ttt acc tgt ata gtg tac ttc atg	1488		
156	Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met			
157	485 490 495			
159	tta gga ttg aag cca aag gca gat gcc ttc ttc gtt atg atg ttt acc	1536		
160	Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr			
161	500 505 510			
163	ctt atg atg gtg gct tat tca gcc agt tcc atg gca ctg gcc ata gca	1584		
164	Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala			
165	515 520 525			
167	gca ggt cag agt gtg gtt tct gta gca aca ctt ctc atg acc atc tgt	1632		
168	Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys			
169	530 535 540			
171	ttt gtg ttt atg atg att ttt tca ggt ctg ttg gtc aat ctc aca acc	1680		
172	Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr			
173	545 550 555 560			
175	att gca tct tgg ctg tca tgg ctt cag tac ttc agc att cca cga tat	1728		
176	Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr			
177	565 570 575			
179	gga ttt acg gct ttg cag cat aat gaa ttt ttg gga caa aac ttc tgc	1776		
180	Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys			
181	580 585 590			
183	cca gga ctc aat gca aca gga aac aat cct tgt aac tat gca aca tgt	1824		
184	Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys			
185	595 600 605			
187	act ggc gaa gaa tat ttg gta aag cag ggc atc gat ctc tca ccc tgg	1872		
188	Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp			
189	610 615 620			
191	ggc ttg tgg aag aat cac gtg gcc ttg gct tgt atg att gtt att ttc	1920		
192	Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe			
193	625 630 635 640			

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203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 2
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215 Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
216          35          40          45
219 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
220          50          55          60
223 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
224 65          70          75          80
227 Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
228          85          90          95
231 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
232          100         105         110
235 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
236          115         120         125
239 Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
240          130         135         140
243 Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
244 145         150         155         160
247 Ile Asn Arg Val Ile Gln Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
248          165         170         175
251 Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
252          180         185         190
255 Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe
256          195         200         205
259 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
260          210         215         220
263 Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
264 225         230         235         240
267 Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
268          245         250         255
271 Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
272          260         265         270
275 Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
276          275         280         285
279 Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
280          290         295         300
283 Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
284 305         310         315         320
287 Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr

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288          325          330          335
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295 Ser Gly Gly Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser
296          355          360          365
299 Tyr Thr Thr Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser
300          370          375          380
303 Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
304 385          390          395          400
307 Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
308          405          410          415
311 Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
312          420          425          430
315 Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe
316          435          440          445
319 Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
320          450          455          460
323 Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
324 465          470          475          480
327 Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
328          485          490          495
331 Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
332          500          505          510
335 Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala
336          515          520          525
339 Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys
340          530          535          540
343 Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr
344 545          550          555          560
347 Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
348          565          570          575
351 Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys
352          580          585          590
355 Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys
356          595          600          605
359 Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
360          610          615          620
363 Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
364 625          630          635          640
367 Leu Thr Ile Ala Tyr Leu Lys Leu Leu Phe Leu Lys Lys Tyr Ser
368          645          650          655

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371 <210> SEQ ID NO: 3

372 <211> LENGTH: 18

373 <212> TYPE: DNA

374 <213> ORGANISM: Artificial Sequence

376 <220> FEATURE:

377 <223> OTHER INFORMATION: Synthetic DNA

379 <400> SEQUENCE: 3

380 gtgccactc aaaaggtt

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VERIFICATION SUMMARY

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